Adopting caBIG® at the University of Arkansas for Medical Sciences

Laura Hutchins, M.D.

From the beginning of the Cancer Center, we've had need for handling large amounts of data. We want to be able to translate the work from the lab to the clinic and from the clinic to the lab, and in order to do that, the two types of data need to be able to speak to each other. They need to connect in some way, and once again that has to be done in a challenging environment to protect patient and subject rights. And it's not going to be possible to unite the people that are necessary to work on these projects without using technology.

Without there being infrastructure that's supported by the campus or elements outside the campus, it leads to what I call "everyman for himself." And that means everybody goes out and figures out their own database—their own support—and that is very costly from an enterprise standpoint. It's also somewhat dangerous because without good backup for the data, you can lose large amounts of work that has been done. So, it's really not the best strategy going forward.

Our Cancer Center is in the process of revamping the software and hardware that we have had supporting our research. And so, the decision was either to go in the direction of a caBIG®-type approach or to go with a vendor. And based on my past experience, I was very excited to find out about all of the applications available through the caBIG® initiative.

Cheryl Lane

We have a variety of the out-of-the-box applications from different vendors. There's just no connectivity, and we would find ourselves needing to make changes and no ability to do that sort of thing. We make those requests back to the vendor, and it may or may not even be possible. So for us, we want our applications to be customized to the point that it enhances and helps the workflow of the clinician or the researcher. If we can't accomplish that, then we're not helping them with their day-to-day activities.

Dr. Laura Hutchins and I attended the caBIG® conference in 2006. We saw open source solutions for clinical trials, and we knew that we needed a solution like that for the Cancer Institute. So, we were very interested in the vision that was being offered by caBIG®, and we knew that we wanted to get involved with that and implement that at our own institution.

Open source meant several things for us. First of all, it meant that it was not a costly initiative for us. We didn't have funding from our enterprise to purchase a clinical trial management set of tools. Additionally, we knew that we were going to be able to do customizations with open source tools. And without the ability to customize, we wouldn't be able to facilitate the clinicians' workflow. caBIG® is going to help us because we did not have an enterprise wide solution for clinical trials, and this is going to provide us with a mechanism to offer that to all of our research community within UAMS.

Thomas Keiber-Emmons, Ph.D.

caBIG® obviously is the great equalizer. That's the way I view this. You do have a concept for standardization. You do have a concept for being a venue for everyone using the right tools. So if this is what we've settled on in the context of leveling the playing field, then people like me have to encourage others to really understand that that's a good direction. It's a question of understanding how to use it in a smart way.

So, if you understand how to use it in a smart way, then the task is to convince others it's in their best interest to follow through and to utilize the same sort of tools. You show by example. Look, this is how it works great for you in this particular case. There's still room for innovation. So, that's another beauty of this—it's not just that it's written and cast in stone. So, there is room. So, if a person is really unhappy with the way a particular person has implemented a particular algorithm, you can just say to them, "Yes, you can make the change. It's okay. It's open source."

Laura Hutchins, M.D.

Right now, we're getting the different groups that function to work on research and IT together by actually solving—attacking a problem. So, for example, we need a database setup for the data for a clinical trial using Dr. Keiber-Emmons breast cancer vaccine. We're getting ready to launch that trial. So, we are sitting down and saying, "Okay, what is that we need?" and we're saying, "What do we have now? What do we need to implement?" And we're using that as the focus because that's the best way to get people to participate is if you're solving a problem that's right there in front of us.

Thomas Keiber-Emmons, Ph.D.

It allows us to almost move on a dime. So, we've done a great job of integrating different components. For example, in our clinical trial suite we were very advanced. Part of it is necessity in the context of developing automated systems for grant transfer information and applying for or moving things up to the IRB and things like that. So, we've wrapped a lot of that stuff around the caBIG® tools. And it's actually been great for us.

Cheryl Lane

For our clinical trial management suite, we want to make the use of that as seamless as possible to the researchers. So, what we've done is we've created a single sign-on dashboard that wraps around C3PR, Patient Study Calendar, and OpenClinica. We additionally are going to be implementing the adverse event tools as well as the Lab Viewer within our Dashboard Suite in the near future.

What we're trying to do is set this up so that the researcher has one more place to go for all the clinical research efforts. We have an electronic RB system that we wrote a number of years ago as well as a budgeting tool that supports protocol submissions. Those, as well as our caBIG® tools, are part of our Dashboard. Once you've logged into the Dashboard, you can move from one module to the next without a loss of functionality.

Laura Hutchins, M.D.

We generate a lot of data that if we just had a way to analyze it could give us leads. Questions come up every day, so thinking about trying to organize our clinical work so that it can be handled almost the same way or flow into some of the caBIG® tools may let us do exploratory analyses in a much more rapid way than we would have them doing it now. At the moment, there aren't any tools that can connect, in a large way, research data with clinical data. And so, caBIG® is one of the first initiatives to be able to do that. And then to be able to capitalize potentially on uniting your data with someone else's data is just going to move the field forward faster.

I think the most developed project is in the Myeloma Institute. And they have patient samples that they do gene array on and use that information to provide patient care as well as develop additional research initiatives. And so, the Myeloma Institute has some specific needs. We're in the process right now of testing the caTissue to see if we can migrate their current tissue banking needs over to caTissue. They have some specific requirements that are different than a normal tissue bank, so that's our starting point. But we plan to expand from there to more or less replace what they've been using at the current time.

Cheryl Lane

In the case of caTissue, they had an existing toolset that they used. For us to understand the needs of the end-user, we really have to sit down not only and listen to their needs but also even go into the clinic areas and to watch their workflow. Often times, it's the support staff of the clinicians or the researchers who do a lot of the data entry. And so, we have to get a sense of what that workflow is in order to do the customization needed for those applications to work properly.

And so, it was literally watching them receive a specimen in the lab and looking at how they then entered that information into their existing application because some of the functionality didn't exist from caTissue when we received it. But because it was open source, it was easy for us to then make those customizations that fit into their workflows.

John Shaughnessy, Jr., Ph.D.

I think what caBIG® and all its tools are going to do is allow more rapid application of questions. With our data now, we come up with a new question almost every single day. And what I find is difficult is compiling all of the data that's necessary to get that question answered in a timely fashion. That's where we're failing, and this is where I think this can help. The caBIG® is going to help in another way is that it's more secure. It's not prone to corruption as much as some other perhaps home brewed datasets are and that when you share the data, it's in a very secure environment.

You've got sixteen different types of multiple myeloma. So, if you've only got 19,000 cases a year— you've got twenty drugs that you want to test—you can do the numbers and see that it's almost going to be impossible to understand if this new drug works in this particular type of myeloma, and you can start mixing and personalizing medicine.

So, that's why there has to be more integration in my view. It's going to be hopeless to get to any type of personalized medicine unless there's some kind of an integration where every patient comes in and gets a molecular profile done. They get that information. It can be put in a clearing house like a caBIG®, for example. And then they get treated and that treatment gets put into the caBIG® archive. And then somebody—the experts in bioinformatics—can come in and say, "Aha! Although this wasn't treated at all in one center, this meta data is going to be what we need to try to do this."

Thomas Keiber-Emmons, Ph.D.

So, part of the desire or the implementation is, again, making people recognize that you may not use all the tools today, but tomorrow you may want something that you didn't have access to. So, not everybody needs to see an image. So, but if you are browsing through something, and all of a sudden it dawns on you that it's probably a good idea to take a look at what this person's tumor looks like—why would you not want to have that capability?

So again, it comes back to that vision. You have to have clinicians. You have to have the IT people. You have to have the bench/translational people advocating that you may not use this today, but tomorrow you're going to find that it's your new best friend.

Interviewees

Laura Hutchins, M.D.
Professor of Medicine and Director of Hematology/Oncology
University of Arkansas for Medical Sciences

Thomas Keiber-Emmons, Ph.D.
Professor of Pathology, Microbiology, and Immunology
Director of Basic Breast Cancer Research
University of Arkansas for Medical Sciences

Cheryl Lane
Director of Information Technology Research and Development Systems
University of Arkansas for Medical Sciences

John Shaughnessy, Jr., Ph.D.
Director of Basic Research
Myeloma Institute

For more information, please visit http://cabig.cancer.gov/.